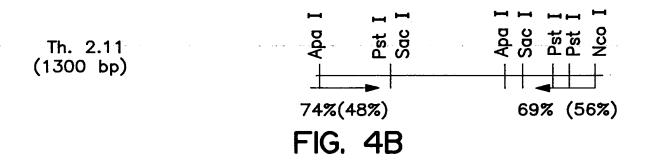


FIG. 4A



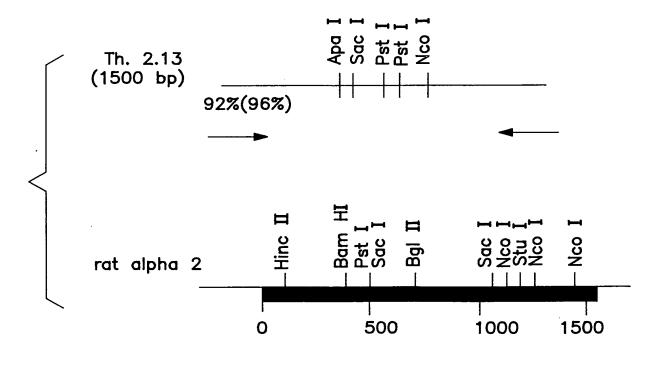
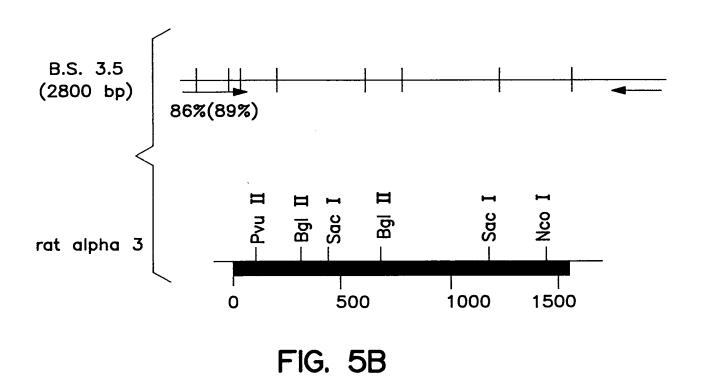


FIG. 4C





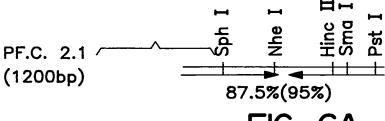


FIG. 6A

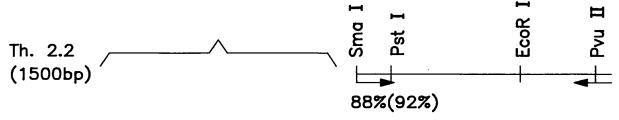
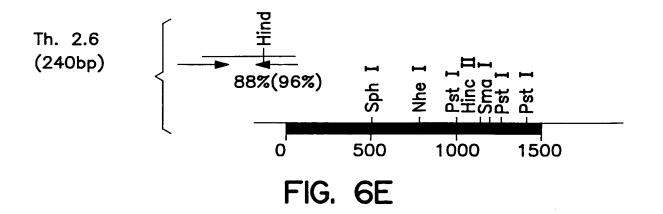


FIG. 6B

FIG. 6C

FIG. 6D



	• • • • • • • • • • • • • • • • • • • •	
195	GCTAAACAGGAGTGGAGCGACTACAAACTGCGCTGGAAC	157
251	CCAATGTCTGGCTAAAGCAGGAATGGAATGACTACAAGCTGCGCTGGGAC	300
156	CCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGAT	107
301	CCGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT	305
301	CCGGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT	303
	BamHI	
106	CTGGATCCCCGACATTGTTCTCTACAACAAAAATGGGGAGTTTGCAG	60
		400
351	CTGGATCCCAGACATTGTCCTCTACAACAATGCAGATGGGGAGTTTGCGG	400
59	TGACCCACATGACCAAGGCCCACCTCTTCTCCACGGGCACTGTGCACTGG	10
401	TGACCCACATGACCAAGGCTCACCTCTTCTTCACGGGCACTGTGCACTGG	450
9	GTGCCCCC	
3	111111	
151	CTCCCCCA	

FIG. 7A

1	CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACTTATG	50
501	CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACATATG	550
51	ACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAG	100
		600
551	ACAAGGCCAAGATCGATCTGGAGCAGATGGAGAGGACAGTGGACCTGAAG	600
101	GACTACTGGGAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTA	150
101		-00
601	GACTACTGGGAGAGTGGCGAGTGGGCCATTATCAATGCCACCGGAACCTA	650
151	CAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTACCCCGACGTCACCT	200
651	TAACAGTAAGAAGTACGACTGCTGCGCGGAGATCTACCCCGATGTCACCT	700
	AG	
201	AG	202
701	, , , , , , , , , , , , , , , , , , ,	750
701	ACTACTTTGTGATCCGGCGGCTGCCGCTGTTCTATACCATCAACCTCATC	750

FIG. 7B

1		31
51		100
32	AGCGGCTGTTTGAAGATTACAATGAGATCATCCGGCCTGTAGCCAACGTG	81
101	AGTACCTGTTCGAAGATTACAACGAGATCATCCGGCCAGTGGCTAATGTG	150
82		131
151	TCCCATCCAGTCATCCAGTTTGAGGTGTCCATGTCTCAGCTGGTGAA	200
132	GGTGGATGAAGTAAACCAGATCATGGAGACCAACCTGTGGCTCAAGCAAA	181
201	GGTGGATGAAGTAAACCAGATCATGGAAACCAACCTGTGGCTGAAGCAAA	250
182	TCTGGAATGACTACAAGCTGAAGTGGAACCCCTCTGACTATGGTGGGGCA	231
251	TCTGGAATGACTACAAGCTGAAATGGAAACCCTCTGACTACCAAGGGGTG	300
232	. BglII GAGTTCATGCGTGTCCCTGCACAGAAGATCTGGAAGCCAGACATTGT	278
301	GAGTTCATGCGTGTTCCTGCAGAGAAGATCTGGAAACCAGACATCGTACT	350

FIG. 8A

1	TTCCAGGTGGACGACAAGACCAAAGCCT	28
351		400
29	TACTCAAGTACACTGGGGACGTGACTTGGATACCTCCGGCCATCTTTAAG	78
401	TACTCAAGTACACAGGAGAAGTGACTTGGATCCCGCCGGCCATCTTTAAG	450
79	SacI AGCTCCTGTAAAATCGACGTGACCTACTTCCCGTTTGATTACCAAAACTG	128
451	AGCTCATGCAAAATCGACGTGACCTACTTCCCATTCGACTACCAAAACTG	500
129	TACCATGAAGTTCGGTTCCTGGTCCTACGATAAGGCGAAAATCGATCTGG	178
501	CACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGG	550
179	TCCTGATCGGCTCTTCCATGAACCTCAAGGACTATTGGGAGAGCGGCGAG	228
551	TCCTCATCGGCTCCTCCATGAACCTCAAGGACTACTGGGAGAGTGGCGAG	600
229	TGGGCCATCATCAAAGCCCCAGGCTACAAACACGACATCAAGTACAACTG	278
601	TGGGCTATCATTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAACTG	650
279	CTGCGAGGAGATCTACCCCGACATCAC	305
651	CTGTGAGGAGATCTACCAAGACATCACGTACTCGCTGTACATCCGTCGCC	700

FIG. 8B

1	ATGCCCGCTGGCATGGCCCGGGCGCTGCGCCCCGTGGCGCTGCTCCTTGG	50
1	ATGCTGGCTTGCATGGCCGGGCACTCCAACTCAATGGCGCTGTTCAG	47
51	CTTCGGCCTCCTCCGGCTGTGCTCAGGGGTGTGGGGTACGGATACAGAGG	100
48		97
101	AGCGGCTGGTGGAGCATCTCCTGGATCCTTCCCGCTACAACAAGCTTATC	150
98	AGCGGCTAGTGGAGCATCTCTTAGATCCCTCCCGCTATAACAAGCTGATT	147
151	CGCCCAGCCACCAATGGCTCTGAGCTGGTGACAGTACAGCTTATGGTGTC	200
148		197
201	ACTGGCCCAGCTCATCAGTGTGCATGAGCGGGAGCAGATCATGACCACCA	250
198		247
251	ATGTCTGGCTGACCCAGGAGTGGGAAGATTATCGCCTCACCTGGAAGCCT	300
248	ATGTCTGGCTGACCCAGGAGTGGGAAGATTACCGCCTCACATGGAAGCCT	297
301	GAAGAGTTTGACAACATGAAGAAAGTTCGGCTCCCTTCCAAACACATCTG	350
248	GAGGACTTCGACAATATGAAGAAAGTCCGGCTCCCTTCCAAACACATCTG	347

FIG. 9A

351	GCTCCCAGATGTGGTCCTGTACAACAATGCTGACGGCATGTACGAGGTGT	400
348	GCTCCCAGATGTGGTTCTATACAACAATGCTGACGGCATGTACGAAGTCT	397
401	CCTTCTATTCCAATGCCGTGGTCTCCTATGATGGCAGCATCTTCTGGCTG	450
398	CCTTCTATTCCAATGCTGTGGTCTCCTATGATGGCAGCATCTTTTGGCTA	447
451	. SphI CCGCCTGCCATCTACAAGAGCGCATGCAAGATTGAAGTAAAGCACTTCCC	500
448	CCACCTGCCATCTACAAGAGTGCATGCAAGATTGAGGTGAAGCACTTCCC	497
501	ATTTGACCAGCAGAACTGCACCATGAAGTTCCGTTCGTGGACCTACGACC	550
498	ATTTGACCAGCAGAATTGCACCATGAAGTTTCGCTCATGGACCTACGACC	547
551	GCACAGAGATCGACTTGGTGCTGAAGAGTGAGGTGGCCAGCCTGGACGAC	600
548	GTACTGAGATTGACCTGGTGCTCAAAAGTGATGTGGCCAGTCTGGATGAC	597
601	TTCACACCTAGTGGTGAGTGGGACATCGTGGCGCTGCCGGGCCGCGCAA	650
598	TTCACACCCAGCGGGAGTGGGACATCATCGCACTGCCAGGCCGACGCAA	647
651	CGAGAACCCCGACGACTCTACGTACGTGGACATCACGTATGACTTCATCA	700
648	CGAGAACCCAGACGACTCCACCTATGTGGACATCACCTATGACTTCATCA	697

FIG. 9B

701	TTCGCCGCAAGCCGCTCTTCTACACCATCAACCTCATCATCCCCTGTGTG	750
698	TTCGTCGCAAACCACTCTTCTACACTATCAACCTCATCATCCCCTGCGTA	747
751	CTCATCACCTCGCTAGCCATCCTTGTCTTCTACCTGCCATCCGACTGTGG	800
748	CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG	797
801	CGAGAAGATGACGTTGTGCATCTCAGTGCTGCTGGCGCTCACGGTCTTCC	850
798		847
851	TGCTGCTCATCTCCAAGATCGTGCCTCCCACCTCCCTCGACGTGCCGCTC	900
848		897
901	GTCGGCAAGTACCTCATGTTCACCATGGTGCTTGTCACCTTCTCCATCGT	950
898		947
951	CACCAGCGTGTGCGTCCTCAACGTGCACCACCGCTCGCCCACCACCACACACA	1000
948		997
1001	CCATGGCGCCTGGGTGAAGGTCGTCTTCCTGGAGAAGCTGCCCGCGCTG	1050
998	CCATGGCCCCTGGGTCAAGGTGGTCTTCCTGGAGAAGCTGCCCACCCTG	1047

FIG. 9C

	CTCTTCATGCAGCCACGCCATCATTGCGCCCGTCAGCGCCTGCGCCT	1100
		1097
1101	GCGGCGACGCCAGCGTGAGCGCGAGGGCGCTGGAGCCCTCTTCTTCCGCG	1150
1098	GAGGAGGCGCCAGCGAGAGCGTGAGGGCGAGGCGGTTTTCTTCCGTG	1144
1151	AAGCCCAGGGGCCGACTCCTGCACGTGCTTCGTCAACCGCGCGTCGGTG	1200
1145	AAGGTCCTGCGGCTGACCCATGTACCTGCTTTGTCAACCCTGCATCAGTG	1194
1201	CAGGGTTGGCCGGGGCCTTCGGGGCTGAGCCTGCACCAGTGGCGGGCCC	1250
1195	CAGGGCTTGGCTGGGGCTTTCCGAGCTGAGCCCACTGCAGCCGGCCC	1241
1251	CGGGCGCTCAGGGGAGCCGTGTGGCTGTGGCCTCCGGGAGGCGGTGGACG	1300
1242	GGGGCGCTCTGTGGGGCCATGCAGCTGTGGCCTCCGGGAAGCAGTGGATG	1291
	GCGTGCGCTTCATCGCAGACCACATGCGGAGCGAGGACGATGACCAGAGC	1350
1292	GCGTACGCTTCATTGCGGACCACATGCGAAGTGAGGATGATGACCAGAGT	1341
1351	GTGAGTGAGGACTGGAAGTACGTCGCCATGGTGATCGACCGCCTCTTCCT	1400
1342	GTGAGGGAGGACTGGAAATACGTTGCCATGGTGATCGACCGCCTGTTCCT	1391

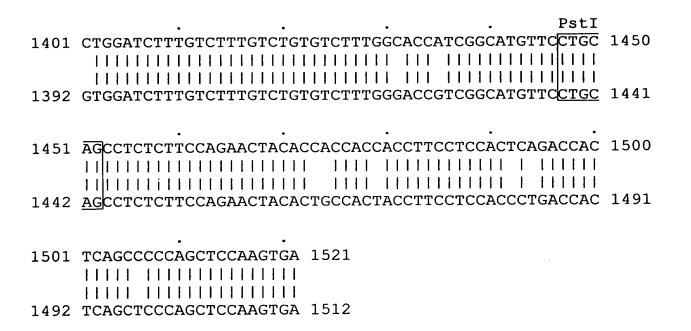


FIG. 9E